

Resource Summary Report

Generated by SPARC SAWG on Sep 16, 2026

Fastahack

RRID:SCR_016090

Type: Tool

Proper Citation

Fastahack (RRID:SCR_016090)

Resource Information

URL: <https://github.com/ekg/fastahack>

Proper Citation: Fastahack (RRID:SCR_016090)

Description: Software application for indexing and extracting sequences and subsequences from FASTA files. It will only generate indexes for FASTA files in which the sequences have self-consistent line lengths.

Resource Type: software application, software resource

Keywords: extract, quickly, subsequence, sequence, FASTA, files, generate, index

Availability: Free, Available for download

Resource Name: Fastahack

Resource ID: SCR_016090

Alternate IDs: OMICS_20516

Alternate URLs: <https://packages.debian.org/stretch/fastahack>,
<https://sources.debian.org/src/fastahack/>

License: MIT license

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260912T200253+0000

Ratings and Alerts

No rating or validation information has been found for Fastahack.

No alerts have been found for Fastahack.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Vromman M, et al. (2022) CIRCprimerXL: Convenient and High-Throughput PCR Primer Design for Circular RNA Quantification. Frontiers in bioinformatics, 2, 834655.